CLAIMS

What Is Claimed Is:

1. A method comprising:

predicting a secondary structure of a protein;

superimposing the predicted secondary structure on a set of topomers;

refining the superimposed secondary structure; and

predicting a tertiary structure of a protein

2. The method of claim 1, wherein said predicted secondary structure is a consensus predicted secondary structure.

3. The method of claim 1, further comprising annealing the secondary structure by energy minimization.

4. The method of claim 3, wherein said energy minimization is by a random Monte Carlo method.

5. The method of claim 4, wherein the random Monte Carlo method uses random moves from a log probability table.

6. The method of claim 3, wherein the random Monte Carlo method uses smart moves.

7. The method of claim 1, wherein the secondary structure superimposed on a set of topomers is refined by energy minimization.

8. The method of claim 7, wherein the secondary structure superimposed on a set of topomers is refined using a molecular modeling program.

9. The method of claim 8, wherein the molecular modeling program is X-PLOR.

10. The method of claim 1, wherein the protein secondary structure is predicted by at least one technique selected from the group consisting of Chou-Fasmand and GOR (Garnier, Osguthorbe and Robson).

11. The method of claim 1, wherein the protein secondary structure is predicted by at least one program selected from the group consisting of PSI-pred, JPRED, Prof, PREDATOR, PHD, ZPRED, nnPredict, BMERC, PSA Server, SSP and PROFsec.

12. The method of claim 1, wherein the set of topomers is derived using Continuous Configuration Boltzman Biased Direct Monte Carlo Method.

13. The method of claim 1, wherein the superimposed secondary structure is refined by a program selected from the group consisting of AMBER, CHARMM, X-PLOR and INSIGHTII.